

Amendments to the Claims

Claims 1-9 (Cancelled)

Claim 10 (Currently amended): A method of screening animals for a genotype associated with litter size and meat quality traits such as color, pH level, marbling, and drip loss, to identifying a pig with a polymorphism at position 199 of SEQ ID NO:2, wherein a pig with an isoleucine at amino acid position 199 when an arginine is at amino acid position 200 in SEQ ID NO:2 is indicative of a pig more likely to have higher ultimate pH and lower glycogen content than a pig with a valine at amino acid position 199 and an arginine at amino acid position 200 in SEQ ID NO:2 or a pig with a valine at position 199 and a glutamine at position 200, wherein a valine at amino acid position 199 and an arginine at position 200 is indicative of a lower ultimate pH and higher glycogen content and wherein a pig with a valine at amino acid position 199 and a glutamine at position 200 is indicative of lower ultimate pH and higher glycogen content, the method comprising:

obtaining a biological sample of material from said animal; and

detecting the amino acid encoded at positions 199 and 200 of SEQ ID NO:2; and

relating the polymorphism to the phenotype.

assaying said sample for a PRKAG3 genotype comprising at least one polymorphic allele,

wherein said PRKAG3 genotype encodes a polypeptide having at least 95% sequence identity to SEQ ID NO:2, and is characterized by a nucleic acid sequence which encodes a polypeptide having an amino acid of valine at position 199 and arginine at position 200,

or an isoleucine at position 199 when an arginine is at position 200 in SEQ ID NO:2 or at an equivalent position in SEQ ID NO:2 when aligned in a Blast comparison using default parameters,

thereby screening for or against animals having said traits.

Claim 11 (Currently amended): The method of claim 10 wherein said polymorphism is a transition of a guanine to an adenine at nucleotide position 595 of SEQ ID NO:1 ~~or a nucleotide sequence having substantial sequence similarity to SEQ ID NO:1 as measured using BLAST sequence comparison algorithm.~~

Claims 12-44 (Cancelled)

Claim 45 (Currently amended): A method ~~of for identifying a pig with a polymorphism at position 199 of SEQ ID NO:2, wherein a pig with a threonine at amino acid position 30, a glycine at amino acid position 52, an isoleucine encoded at amino acid position 199 in SEQ ID NO:2 is indicative of a pig more likely to have a higher ultimate pH and lower color scores than a pig with a threonine at amino acid position 30, a glycine at amino acid position 52, and a valine at amino acid position 199 in SEQ ID NO:2, wherein a threonine at amino acid position 30, a glycine at amino acid position 52, and a valine at amino acid position 199 is indicative of a lower ultimate pH and higher color scores, screening animals to determine those more likely to have favorable meat quality traits.~~ the method comprising:
detecting the amino acid encoded at positions 30, 52, and 199 of SEQ ID NO:2; and
relating the polymorphism to the phenotype.
~~obtaining a sample of biological material from an animal;~~
~~assaying the PRKAG3 protein in said sample, wherein said protein has at least 95% sequence identity to SEQ ID NO:2 and is characterized by for a threonine at amino acid position 30, a glycine at amino acid position 52 and an isoleucine at amino acid position 199 in SEQ ID NO:2 or at an equivalent position when aligned to SEQ ID NO:2 in a Blast comparison using default parameters, wherein the presence of said threonine at amino acid position 20, glycine at amino acid position 52 and isoleucine at amino acid position 199 is indicative of said animal possessing favorable meat quality traits comprising color, pH level, marbling, and drip loss.~~

Claims 46-55 (Cancelled)

Claim 56 (Currently amended): ~~A method of screening animals for identifying a pig to determine with a these polymorphism at position 52 of SEQ ID NO:2, wherein a pig with a threonine at amino acid position 30, a serine at amino acid position 52 and a valine at amino acid position 199 in SEQ ID NO:2 is indicative of a pig more likely to have favorable meat quality traits a higher ultimate pH and lower color scores than a pig having a theronine at amino acid position 30, a glycine at amino acid position 52, and a valine at amino acid position 199 in SEQ ID NO:2, wherein a theronine at amino acid position 30, a glycine at amino acid position 52, and a valine at amino acid position 199 is indicative of a lower ultimate pH and higher color scores, the method comprising:~~

~~obtaining a sample of biological material from an animal; and~~

~~assaying from said sample the PRKAG3 protein for amino acid changes in said animal which are associated with favorable meat quality traits comprising color, pH level, marbling, and drip loss, said amino acid changes are characterized by a threonine at amino acid position 30, a serine at amino acid position 52 and a valine at amino acid position 199 in SEQ ID NO:2 or at an equivalent position as measured by a Blast comparison using default parameters~~

~~detecting the amino acid at positions 30, 52, and 199 of SEQ ID NO:2; and~~

~~relating the polymorphism to the phenotype.~~

Claims 57-60 (Cancelled)